AMENDMENTS

Please amend claims 87 and 88 as follows:

87. (Twice Amended) A primer molecule having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the specificity region defined as one of all possible sequence combinations of A, T, G and C.

88. (Twice Amended) A population of primer molecules, the primer molecules having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the population of primer molecules having specificity regions collectively reflecting all possible sequence combinations of A, T, G and C.

REMARKS AND RESPONSE TO OFFICIAL ACTION

I. Claims in the Case

Claims 87-88 have been amended. Claims 3, 4, 20, 21, 23-29, 36-76 and 85-89 are pending.

II. Rejection of Claims 87-89 Under Section 102(b)/103 over Senapathy

The Action first takes the position that the subject matter of claims 87-89 are anticipated or obvious over the Senapathy '058 patent. The Action's position is that Senapathy teaches a DNA molecule wherein the 3' end is degenerate, comprising all combinations of sequence possibilities, and the 5' end comprises a sequence that is complementary to a known sequence, thus permitting subsequent amplification. The Action explicitly recognizes that Senapathy does

not teach that the predetermined 5' end should be complementary to a known linker sequence. Rather, the Action takes the position that the since the claims are set forth in intended use format, they somehow inherently anticipate structures wherein the 5' end is "capable" of binding to a known linker sequence. The Applicants respectfully traverse.

Claims 87-89 were directed to primer molecules having a predetermined sequence at their 5' ends "for annealing to a linker sequence." However, the Action concedes that Senapathy only provides an explicit disclosure of structures that have a predetermined 5' sequence for hybridizing to some known sequence, but nothing about a predetermined sequence that anneals to a ***linker*** as required by the present claims. The Action has not pointed to any disclosure from Senapathy to suggest that this region could or should have a sequence that will serve to hybridize to a known linker, and the Applicants have been unable to identify any such teaching or suggestion. While the Action appears to implicitly recognize the distinction between a linker sequence, on the one hand, and, for example, a primer sequence on the other, the Action nevertheless argues that the claims are set forth in intended use format and thus cannot distinguish over the art as written.

In response, Applicants have proceeded to amend claims 87 and 88 to make it clear that the claim now requires a predetermined 5' sequence that comprises a sequence that anneals to a ***linker*** having a predetermined sequence. As such, the claims now identify subject matter that is novel and non-obvious over Silver.

III. Rejection of Claims 87-89 Under Section 102(a)/103 over Silver

The Action next takes the position that the subject matter of claims 87-89 are anticipated or obvious over the Silver '792 patent. The Action's position is that Silver teaches a DNA

molecule wherein the 3' end is degenerate, comprising all combinations of sequence possibilities, and the 5' end comprises a sequence that is complementary to a primer, thus permitting subsequent amplification. The Action implicitly recognizes that a "primer sequence" is not the same as a "linker sequence" (as required by the claims) but argues that such is somehow inherent in the disclosure of Silver. The Applicants respectfully traverse.

Claims 87-89 were directed to primer molecules having a predetermined sequence at their 5' ends "for annealing to a linker sequence." However, it appears that Silver only concerns primers that have a predetermined 5' sequence that hybridizes to an amplification ***primer***, and says nothing about a predetermined sequence that hybridizes to a ***linker*** as required by the present claims. For example, Silver states, at col. 1, lns 31-33, that "all of" the primers of the Silver invention "share the same 5' end sequence for a distance long enough to serve as a ***primer*** in a subsequent PCR reaction ..." (emphasis supplied) The Action has not pointed to any disclosure from Silver to suggest that this region could or should have a sequence that will serve to hybridize to a known linker, and Applicants have been unable to identify any such teaching or suggestion. While the Action appears to implicitly recognize the distinction between a linker sequence, on the one hand, and a primer sequence on the other, the Action nevertheless argues that the claims are set forth in intended use format and thus cannot distinguish over the art as written.

In response, Applicants have proceeded to amend claims 87 and 88 to make it clear that the claim now requires a predetermined 5' sequence that comprises a sequence that anneals to a ***linker*** having a predetermined sequence. As such, the claims now identify subject matter that is novel and non-obvious over Silver.

IV. Nonstatutory Double Patenting Rejection

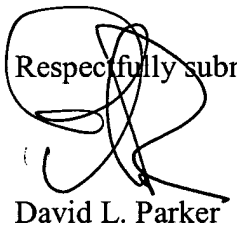
Lastly, the Action next rejects claims 3-4, 20, 21, 23-29, 36-49, 52-76, 85 and 87-89 under the judicially created doctrine of obviousness type double patenting over the parent '600 patent.

Curiously, the Action provides no explanation as to how or why the rejection is appropriate. As such, the Action has failed to satisfy its prima facie burden. Nevertheless, while it is entirely unclear how such a rejection is appropriate, Applicants are willing to submit a terminal disclaimer, since such would have no effect on the pendency of any patent that might subsequently issue. An appropriate terminal disclaimer is enclosed.

V. Conclusion

It is submitted that the present response is a complete response to the outstanding official action, and that the claims are in condition for allowance. If the Examiner has any questions or comments, a telephone call to the undersigned at (512) 536-3055 is requested.

Respectfully submitted,



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CLAIM AMENDMENTS

87. (Twice Amended) A primer molecule having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined ~~for annealing to a~~ linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the specificity region defined as one of all possible sequence combinations of A, T, G and C.

88. (Twice Amended) A population of primer molecules, the primer molecules having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined ~~for annealing to a~~ linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the population of primer molecules having specificity regions collectively reflecting all possible sequence combinations of A, T, G and C.

CURRENTLY PENDING CLAIMS

3. The method of claim 20, wherein said DNA is non-genomic DNA.

4. The method of claim 20, wherein said DNA is cDNA.

20. A method of subjecting a DNA molecule to a DNA synthesis reaction, comprising the steps of:

a) obtaining a DNA molecule having a first linker sequence positioned at one end of the DNA molecule and a second linker sequence, different from said first linker sequence, positioned at the other end of the DNA molecule; and

b) subjecting said DNA to a DNA synthesis reaction with a primer set comprising:

i) a first primer, wherein the 5' sequence of said primer is complementary to said first linker sequence and the 3' sequence of said primer comprises a specificity region; and

ii) a second primer, wherein the 5' sequence of said primer is complementary to said second linker sequence and the 3' sequence of said primer comprises a specificity region.

21. The method of claim 85, wherein said amplification is performed with an array of combinations of alternate amplification primers.

23. The method of claim 85, further comprising, identifying the amplified DNA.

24. The method of claim 23, wherein said identification is based upon length.

25. The method of claim 23, wherein said identification is performed by a computer program.

26. The method of claim 21, wherein said array of amplifications is performed in a multi-well plate.

27. The method of claim 20, wherein the specificity region of the primers of the first primer set is 3,4,5,6,7 or 8 base pairs long.

28. The method of claim 20, wherein the specificity region of the primers of the second primer set is 3,4,5,6,7 or 8 base pairs long.

29. The method of claim 85, wherein said amplification comprises polymerase chain reaction, nucleic acid sequence based amplification, transcription mediated amplification, strand displacement amplification or ligase chain reaction.

36. The method of claim 85, wherein a label is incorporated into said amplified DNA.

37. The method of claim 36, wherein said label is incorporated by means of a labeled primer.

38. The method of claim 36, further comprising, partial nucleotide sequence identification of the amplified products by the identity of the label.

39. The method of claim 36, wherein said label is a chromophore.

40. The method of claim 36, wherein said label is a fluorophore.

41. The method of claim 36, wherein said label is an affinity label.

42. The method of claim 36, wherein said label is a dye.

43. The method of claim 37, wherein the 5' end of said primer comprises an amino moiety and a flurophore is covalently attached by the reaction of a succinimido ester of the flurophore to the 5' amino-modified primer.

44. The method of claim 40, wherein said fluorophore is Alexa 350, Alexa 430, AMCA, BODIPY 630/650, BODIPY 650/665, BODIPY-FL, BODIPY-R6G, BODIPY-TMR, BODIPY-TRX, Cascade Blue, Cy2, Cy3, Cy5,6-FAM, Fluorescein, HEX, 6-JOE, Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, REG, Rhodamine Green, Rhodamine Red, ROX, TAMRA, TET, Tetramethylrhodamine, and Texas Red.

45. The method of claim 20, wherein the products of said DNA synthesis reaction are analyzed.

46. The method of claim 45, wherein said analysis of products is by polyacrylamide gel electrophoresis.

47. The method of claim 45,wherein said analysis of products is by capillary gel electrophoresis.

48. The method of claim 45, wherein said analysis of products is by mass spectrophotometry.

49. The method of claim 45, wherein said analysis of products is by energy transfer.

50. The method of claim 45, wherein said analysis of products is by a filtration and extraction device.

51. The method of claim 45, wherein said analysis of products is by the use of interlaced lasers and multiple fluorescent measurements.

52. The method of claim 45, wherein said analysis of products comprises quantifying amplification products.

53. The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a co-amplified reference-gene.

54. The method of claim 52, wherein said quantifying is by measuring the ratio of each product to a panel of reference-genes.

55. The method of claim 52, wherein said analysis of products is by Real-Time PCR.

56. The method of claim 45, wherein said analysis of products is performed in a multi-well plate.

57. The method of claim 45, wherein said analysis of products is performed on a membrane.

58. The method of claim 45, wherein said analysis of products is performed on a solid matrice.

59. The method of claim 58, wherein said solid matrice is a DNA chip.

60. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a different cell or tissue.

61. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cancerous cell or tissue.

62. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a pharmaceutical compound.

63. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a teratogenic compound.

64. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a carcinogenic compound.

65. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a toxic compound.

66. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a biological response modifier.

67. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a hormone, a hormone agonist or a hormone antagonist.

68. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a cytokine.

69. The method of claim 20, performed on DNA derived from a normal cell or tissue and on DNA derived from a cell or tissue treated with a growth factor.

70. The method of claim 20, performed on DNA derived from a normal cell or tissue and on the DNA derived from a cell or tissue treated with the ligand of a known biological receptor.

71. The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue type obtained from different species.

72. The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue type obtained from different organisms.

73. The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue at different stages of development.

74. The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a normal cell or tissue and derived from a cell or tissue that is diseased.

75. The method of claim 20, performed on more than one sample of DNA, wherein the DNA samples are derived from a cell or tissue cultured in vitro under different conditions.

76. The method of claim 20, performed on the DNA derived from a cell or tissue from two organisms of the same species with a known genetic difference.

85. The method of claim 20, wherein the first and second primers are employed to amplify the DNA molecule.

86. The method of claim 20, wherein the first and second primers are employed to sequence the DNA molecule

87. A primer molecule having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the specificity region defined as one of all possible sequence combinations of A, T, G and C.

88. A population of primer molecules, the primer molecules having (a) a predetermined 5' sequence that is prepared to incorporate a sequence that anneals to a predetermined linker sequence and (b) a 3' terminal specificity region of from 3 to 8 nucleotides in length, the population of primer molecules having specificity regions collectively reflecting all possible sequence combinations of A, T, G and C.

89. A primer molecule selected from the population of claim 88.